

2570
7206

#3

ENTERED



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RAW SEQUENCE LISTING

DATE: 02/24/2003

PATENT APPLICATION: US/09/770,564

TIME: 10:15:32

Input Set : N:\Crif3\RULE60\09770564.raw.txt

Output Set: N:\CRF4\02242003\I770564.raw

```

4 <110> APPLICANT: Crasta, Oswald R.
5     Duvick, Jonathan P.
6     Folkerts, Otto
7     Gilliam, Jacob T.
8     Maddox, Joyce R.
11 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase
12     Polynucleotides and Related Polypeptides and Methods of Use
15 <130> FILE REFERENCE: 0875
17 <140> CURRENT APPLICATION NUMBER: US 09/770,564
18 <141> CURRENT FILING DATE: 2001-01-26
20 <150> PRIOR APPLICATION NUMBER: US 09/352,168
21 <151> PRIOR FILING DATE: 1999-07-12
23 <150> PRIOR APPLICATION NUMBER: 60/092,936
24 <151> PRIOR FILING DATE: 1998-07-25
26 <160> NUMBER OF SEQ ID NOS: 33
28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 372
32 <212> TYPE: DNA
33 <213> ORGANISM: Exophiala spinifera.
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (346)...(346)
38 <223> OTHER INFORMATION: n = A,T,C or G
40 <400> SEQUENCE: 1
41   gggccccggc gttctcgtag gctgcgcgga gttggtccca gacagacttt tgctgtacct      60
42   gcttggaactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc      120
43   attgtcgatc gacgtcgatg ctggtatctc tggcaaata gaatgggggtca cagctcgatt      180
44   ggaggacgcc cgagaagcct tggtcgcgcc accacggctt gtcccatacg aagactatct      240
45   tgctatagta gccacaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg      300
W--> 46   gtgaaaatgt caaggtggga tacaagggtt tcggtaacga aaccancacc tttttgcttc      360
47   ggaacacggc gc                                     372
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 182
51 <212> TYPE: DNA
52 <213> ORGANISM: Exophiala spinifera.
54 <400> SEQUENCE: 2
55   gaattttccg ccaatgcttg cttctcggcg ggaagaggtg gtgaaaatgt caaggtggga      60
56   tacaagggtt tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc      120
57   gatcgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc      180
58   ac                                             182
60 <210> SEQ ID NO: 3
61 <211> LENGTH: 29

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Input Set : N:\Crf3\RULE60\09770564.raw.txt

Output Set: N:\CRF4\02242003\I770564.raw

```

62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE, N21965
68 <400> SEQUENCE: 3
69   tggtttcggt accgacaacc ttgtatccc                               29
71 <210> SEQ ID NO: 4
72 <211> LENGTH: 28
73 <212> TYPE: DNA
74 <213> ORGANISM: Artificial Sequence
76 <220> FEATURE:
77 <223> OTHER INFORMATION: Desiged oligonucleotide for 5' RACE, N21968
79 <400> SEQUENCE: 4
80   gagttggtcc cagacagact tttgtcgt                               28
82 <210> SEQ ID NO: 5
83 <211> LENGTH: 1389
84 <212> TYPE: DNA
85 <213> ORGANISM: Exophiala spinifera
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (1)...(1386)
91 <400> SEQUENCE: 5
92   gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg       48
93   Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
94   1      5      10      15
96   gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt       96
97   Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
98   20      25      30
100  gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt       144
101  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
102  35      40      45
104  ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac       192
105  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
106  50      55      60
108  agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag       240
109  Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
110  65      70      75      80
112  ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac       288
113  Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
114  85      90      95
116  ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag       336
117  Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
118  100     105     110
120  gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc       384
121  Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
122  115     120     125
124  gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg       432
125  Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
126  130     135     140

```

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Input Set : N:\Crf3\RULE60\09770564.raw.txt

Output Set: N:\CRF4\02242003\I770564.raw

128	ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
129	Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
130	145 150 155 160	
132	cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
133	Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
134	165 170 175	
136	gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
137	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
138	180 185 190	
140	agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
141	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
142	195 200 205	
144	cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg	672
145	Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met	
146	210 215 220	
148	tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct	720
149	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala	
150	225 230 235 240	
152	gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc	768
153	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly	
154	245 250 255	
156	gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg	816
157	Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu	
158	260 265 270	
160	tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca	864
161	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	
162	275 280 285	
164	ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta	912
165	Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val	
166	290 295 300	
168	tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa	960
169	Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln	
170	305 310 315 320	
172	tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008
173	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
174	325 330 335	
176	gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
177	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
178	340 345 350	
180	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104
181	Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
182	355 360 365	
184	caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152
185	Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
186	370 375 380	
188	gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga	1200
189	Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	
190	385 390 395 400	
192	gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg	1248

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Output Set: N:\CRF4\02242003\I770564.raw

```

193  Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
194              405                      410                      415
196  gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg      1296
197  Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
198              420                      425                      430
200  tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa      1344
201  Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
202              435                      440                      445
204  cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca      1386
205  Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
206              450                      455                      460
208  tag      1389
210 <210> SEQ ID NO: 6
211 <211> LENGTH: 462
212 <212> TYPE: PRT
213 <213> ORGANISM: Exophiala spinifera
215 <400> SEQUENCE: 6
216  Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
217    1              5              10              15
218  Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
219              20              25              30
220  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
221              35              40              45
222  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
223              50              55              60
224  Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
225              65              70              75              80
226  Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
227              85              90              95
228  Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
229              100             105             110
230  Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
231              115             120             125
232  Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
233              130             135             140
234  Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
235              145             150             155             160
236  Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
237              165             170             175
238  Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
239              180             185             190
240  Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
241              195             200             205
242  Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
243              210             215             220
244  Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
245              225             230             235             240
246  Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
247              245             250             255

```

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Output Set: N:\CRF4\02242003\I770564.raw

```

248  Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
249              260              265              270
250  Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
251              275              280              285
252  Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
253              290              295              300
254  Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
255              305              310              315              320
256  Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
257              325              330              335
258  Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
259              340              345              350
260  Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
261              355              360              365
262  Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
263              370              375              380
264  Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
265              385              390              395              400
266  Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
267              405              410              415
268  Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
269              420              425              430
270  Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
271              435              440              445
272  Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
273              450              455              460

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275 <210> SEQ ID NO: 7

276 <211> LENGTH: 1442

277 <212> TYPE: DNA

278 <213> ORGANISM: Exophiala spinifera

280 <220> FEATURE:

281 <221> NAME/KEY: CDS

282 <222> LOCATION: (1)...(646)

284 <221> NAME/KEY: intron

285 <222> LOCATION: (647)...(699)

W--> 287 <221> CDS

288 <222> LOCATION: (700)...(1439)

W--> 290 <400> 7

```

291  gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg      48
292  Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
293   1              5              10              15
295  gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt      96
296  Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
297              20              25              30
299  gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt      144
300  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
301              35              40              45
303  ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac      192
304  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/24/2003
PATENT APPLICATION: US/09/770,564 TIME: 10:15:33

Input Set : N:\Crf3\RULE60\09770564.raw.txt
Output Set: N:\CRF4\02242003\I770564.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 346

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:18,20,24,25,26,27,28,29,30,31,32,33

VERIFICATION SUMMARY

DATE: 02/24/2003

PATENT APPLICATION: US/09/770,564

TIME: 10:15:33

Input Set : N:\Crf3\RULE60\09770564.raw.txt

Output Set: N:\CRF4\02242003\I770564.raw

L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300
L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:290 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:555 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:802 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:1044 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1048 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1052 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1343 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1350 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1351 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1353 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1816 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1820 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1824 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1828 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1832 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1835 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1839 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:2102 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
ORGANISM:Unknown
L:2102 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:2102
L:2240 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:2244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2248 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2252 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2256 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2259 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2263 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2523 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Unknown
L:2523 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:2523
L:2660 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:2663 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2667 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2671 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2675 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2679 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2683 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2994 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
ORGANISM:Unknown
L:2994 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Unknown
L:2994 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:2994
L:3158 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3159 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3161 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3165 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3169 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09770564.raw.txt

Output Set: N:\CRF4\02242003\I770564.raw

L:3180 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3491 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>
ORGANISM:Unknown
L:3491 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Unknown
L:3491 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:3491
L:3654 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3657 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3661 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3665 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3669 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3673 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3888 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:33, <213>
ORGANISM:Unknown